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(71) Applicant: **Affymetrix, Inc.**
Santa Clara, CA 95051 (US)

(72) Inventors:
- **Chee, Mark**
  Palo Alto California 94306 (US)
- **Berno, Anthony**
  San Jose California 95112 (US)
- **Yang, Robert**
  San Romon California 94583 (US)

(74) Representative: **Bizley, Richard Edward et al**
Hepworth, Lawrence, Bryer & Bizley
Merlin House
Falconry Court
Baker's Lane
Epping Essex CM16 5DQ (GB)

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(54) Polymorphisms in human mitochondrial nucleic acid

(57) The invention provides novel human mitochondrial polymorphisms, and probes and primers for detecting the same. Detection of such polymorphisms is useful in a variety of fields such as forensic analysis, epidemiology and preventive medicine.

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Description

The present invention relates to polymorphisms in human mitochondrial nucleic acid and in particular to a segment of human mitochondrial DNA or RNA, an allele-specific oligonucleotide that hybridises to said nucleic acid including said polymorphism, an isolated nucleic acid comprising a segment of a human mitochondrial sequence having a polymorphic site and a method of analysing nucleic acid.

BACKGROUND

Human mitochondrial DNA (mtDNA) is information-rich, encoding some 22 tRNAs, a 12S and a 16S rRNA, and 13 polypeptides involved in oxidative phosphorylation. No introns have been detected. RNAs are processed by cleavage at tRNA sequences, and polyadenylated posttranscriptionally. In some transcripts, polyadenylation also creates the stop codon, illustrating the parsimony of coding.

A complete prototypical sequence of the human mitochondrial genome has been published. See Anderson et al., *Nature* 290, 457-465 (1981). The reported sequence in 16,569 base pairs long. There is strand asymmetry in the base compositions, with one strand (Heavy) being relatively G rich, and the other strand (Light) being C rich. The L strand is 30.9% A, 31.2% C, 13.1% G, and 24.7% T. The sequence of the L-strand is numbered arbitrarily from the MboI-5/7 boundary in the D-loop region.

A human cell may have several hundred or more mitochondria, each with more than one copy of mtDNA. Hence each cell actually contains a population of mtDNA molecules. In many individuals, the mtDNA sequence is essentially clonal. However, some individuals carry more than one mtDNA sequence, a condition known as heteroplasmy. The degree of heteroplasmy can vary from tissue to tissue. Also, the rate of replication of mtDNAs can differ and together with random segregation during cell division, can lead to changes in heteroplasmy over time.

Mitochondrial DNA is maternally inherited, and has a mutation rate estimated to be tenfold higher than single copy nuclear DNA (Brown et al., *Proc. Natl. Acad. Sci. USA* 76, 1967-1971 (1979)). Over 80% of substitutions are transitions (i.e., pyrimidine-pyrimidine or purine-purine).

The determination of a complete human mitochondrial DNA sequence over 15 years ago has had a tremendous influence on studies of human origins and evolution, and the role of mutations in degenerative diseases. Cann et al. *Nature* **325**, 31-36 (1987); Zeviani, et al., *Am. J. Hum. Genet.* **47**, 904-914 (1990); Wallace, *Annu. Rev. Biochem.* **61**, 1175-1212 (1992); Horai et al., *Proc. Natl. Acad. Sci. USA* **92**, 532-536 (1995); Hutchin & Cortopassi, *Proc. Natl. Acad. Sci. USA* **92**, 6892-6895 (1995). Because of the cost and difficulty of conventional sequence analysis, most sequencing studies have focused only on two small hypervariable regions totalling ~600 bp. Greenberg et al. *Gene* **21**, 33-49 (1983); Aquardo & Greenberg, *Genetics* **103**, 287-312 (1983).

The present application describes sequencing of the complete mitochondrial genome of several individuals and identifies a large set of polymorphisms.

SUMMARY OF THE INVENTION

In one aspect, the invention provides nucleic acids comprising segments of human mitochondrial DNA or RNA of between 10 and 100 bases. The segments include any one of the 182 polymorphic sites shown in Table 1. Also included are nucleic acids comprising complements of these segments. In some segments, the polymorphic site is occupied by the base described by Anderson et al., supra. In other segments, the site is occupied by a different base, particularly one of the alternative forms shown in Table 1, column 2, or 4-11.

The invention further provides allele-specific oligonucleotides for analysis of the polymorphic sites shown in Table 1. The allele specific oligonucleotides hybridize to a segment of human mitochondrial nucleic acid or its complement including a polymorphic site shown in Table 1, column 1. Such oligonucleotides can be used as probes or primers.

The invention further provides isolated nucleic acids comprising a segment of the human mitochondrial sequence described by Anderson et al., *Nature* 290, 457-465 (1981), or the complement thereof, including a polymorphic site shown in Table 1, column 1. In these nucleic acids, the polymorphic site within the segment is occupied by a base other than the base shown in Table 1, column 3 ("asn base").

The invention further provides methods of analyzing a nucleic acid. Such methods entail obtaining a mitochondrial nucleic acid from an individual, and determining a base occupying any one of the polymorphic sites shown in Table 1.

BRIEF DESCRIPTION OF THE FIGURES

Fig. 1. (A) Design of a 4L tiled array. Each position in the target sequence (upper case) is queried by a set of 4 probes on the chip (lower case), id ntical except at a single position, termed the substitution position, which is either A, C, G, or T (blue indicates complementarity, red a mismatch). Two sets of prob s are shown, querying adjacent

positions in the target. **(B)** Effect of a change in the target sequence. The probes are th same as in panel A, but the target now contains a single base substitution (C, shown in green). The probe set querying the changed base still has a perfect match (th G probe). However, probes in adjacent sets that overlap the altered target position now have either one or two mismatches (red), instead of zero or one, since they were designed to match the target shown in panel A. **(C)** Hybridization to a 4L tiled array and detection of a base change in the target. The array shown was designed to the mt1 sequence. (Upper panel) hybridization to mt1. The substitution used in each row of probes is indicated to the left of the image. The target sequence can be read 5' to 3' from left to right as the compl ment of the substitution base with the brightest signal. With hybridization to mt2 (lower panel), which differs from mt1 in this region by a T -> C transition, the G probe at position 16,493 is now a perfect match, with the other three probes having single base mismatches (A 5, C 3, G 37, T 4 counts). However, at flanking positions, the probes have either single or double base mismatches, since the mt2 transition now occurs away from the query position.

Fig. 2. Detection of base differences in a 2.5 kb region by comparison of scaled P^0 hybridization intensity patterns between a sample (green) and a reference (red). **(A)** Comparison of ief007 to mt1. In the region shown, there is a single base difference between the two sequences, located at position 16,223 (mt1 C; ief007 T). This results in a "footprint" spanning ~ 20 positions, 11 to the left and 8 to the right of position 16,223, in which the ief007 P^0 intensities are decreased by a factor of more than 10 on average relative to the mt1 intensities. The predicted footprint location is indicated by the gray bar, and the location of the polymorphism is shown by a vertical black line within the bar. **(B)** Comparison of ha001 to mt1. The ha001 target has 4 polymorphisms relative to mt1. The P^0 intensity pattern clearly shows two regions of difference between the targets. Each region contains at least 2 differences, because in both cases the footprints are longer than 20 positions, and therefore are too extensive to be explained by a single base difference. The effect of competition can be seen by comparing the mt1 intensities in the ief007 and ha001 experiments: the relative intensities of mt1 are greater in panel B where ha001 contains P^0 mismatches but ief007 does not. **(C)** The ha004 sample has multiple differences to mt1, resulting in a complex pattern extending over most of the region shown. Thus, differences are clearly detected. Because hybridization intensities are extremely sequence dependent, each of the mitochondrial sequences can also be identified simply by its hybridization pattern.

Fig. 3. Human mitochondrial genome on a chip. **(A)** An image of the array hybridized to a 16.6 kb L strand mitochondrial target RNA. The 16,569 bp map of the genome is shown and the H strand origin of replication (O_H), located in the control region, is indicated. **(B)** A portion of the hybridization pattern, magnified. In each column there are 5 probes: A, C, G, T and D, from top to bottom. The D probe has a single base deletion instead of a substitution, and hence is 24 instead of 25 bases in length. The scale is indicated by the bar beneath the image. Although there is considerable intensity variation, most of the array can be read directly. The image was collected at a resolution of ~ 100 pixels per probe cell. **(C)** The ability of the array to detect and read single base differences in a 16.6 kb sample is illustrated. Two different target sequences were hybridized in parallel to different chips. The hybridization patterns are compared for four different positions in the sequence. Only the $P^{25,13}$ probes are shown. The top panel of each pair shows the hybridization of the mt3 target, which matches the chip P^0 sequence at these positions. The lower panel shows the pattern generated by a sample from a patient with Leber's hereditary optic neuropathy (LHON). Three known pathogenic mutations, LHON3460, LHON4216, and LHON13708, are clearly detected. For comparison, the fourth panel in the set shows a region around position 11,778 that is identical in both samples.

DEFINITIONS

Nucleic acids, including oligonucleotides, can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. Preferred oligonucleotides of the invention include segments of DNA, or their complements including any one of the polymorphic sites shown in Table 1. The segments are usually between 5 and 100 bases, and often between 5-10, 5-20, 10-20, 10-50, 20-50 or 20-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in Table 1.

Hybridization probes are oligonucleotides capable of binding in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

The term primer refers to a single-stranded oligonucleotide capable of acting as a point of initiation of template-directed DNA synthesis under appropriate conditions *(i.e.,* in the presence of four different nucleoside triphosphates and an agent for polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer but typically ranges from 15 to 30 nucleotides. Short primer molecules g n rally requir cooler temperatures to form sufficiently stable hybrid complexes with th template. A primer n ed not reflect the exact sequence of th template but must be sufficiently complementary to hybridize with a template. The term primer site refers to the area of the target DNA to which a primer hybridizes. Th term primer pair means a set of primers including a 5' upstr am prim r that hybridizes

with the 5' end of the DNA sequenc to be amplified and a 3', downstream primer that hybridizes with th complement of the 3' end of the sequence to be amplified.

Linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same chromosome, and can b measured by percent r combination between the two genes, alleles, loci or genetic markers.

Polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as a the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two forms. A triallelic polymorphism has three forms.

A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridizations.

An isolated nucleic acid means an object species invention that is the predominant species present (*i.e.*, on a molar basis it is more abundant than any other individual species in the composition). Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present. Most preferably, the object species is purified to essential homogeneity (contaminant species cannot be detected in the composition by conventional detection methods).

DETAILED DESCRIPTION

I. Novel Polymorphisms of the Invention

The present application provides the location of 505 polymorphisms at 182 sites in human mitochondrial DNA (see attached Table 1). The first column of the table identifies the position of polymorphisms according to a convention whereby nucleotides in the mitochondrial genomes of different individuals are assigned the same number as the corresponding nucleotide in the sequence of Anderson et al., *supra* when the two sequences are maximally aligned. For example, reading from the top of the table, polymorphisms occur at positions 63, 72, 92, 181, 194 and so on. The column headed rbase indicates the base occupying the position in a mitochondrial reference sequence whose sequence was determined by ABI sequencing. The column headed asn-base indicates the base occupying the position in the published sequence of Anderson et al. (1981), *supra*. The remaining columns in the table indicate the base present at the polymorphic position in each of 10 African individuals (designated from left to right HA001, HA002, HA004 and so forth). Upper case letters indicate that the base occupying a polymorphic position has been established with substantial certainty in an individual. Lower case letters indicate that although the existence of a polymorphic position is certain, there is a possibility of experimental error in determining the base indicated as occupying that position in an individual. The letter "n" indicates that the base occupying a position in an individual was ambiguous. Some ambiguities may be due to heteroplasmy.

The polymorphic sites listed in the table are widely distributed throughout the mitochondrial genome, and occur in many of the known genes within the genome (i.e., 22 tRNAs, a 12S and a 16S rRNA, and 13 polypeptides involved in oxidative phosphorylation). The polymorphic sites can be classified in sets according to which gene the polymorphic site occurs.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid from an individual being analyzed. For assay of mitochondrial DNA, virtually any biological sample is suitable. For example, convenient tissue samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair.

Amplification of nucleic acids from target samples is sometimes desirable and can be accomplished by e.g., PCR. *See generally PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202 (each of which is incorporated by reference for all purposes).

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

Amplification is not always necessary in view of the multiple copies of mitochondrial DNA in a single cell. Analysis without amplification is preferred for analysis of relative levels of various mitochondrial DNA subpopulations, such as mitochondrial DNAs bearing deletions, without affecting their relative levels.

B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis depending whether a polymorphism in question has already been characterized. The first type of analysis is sometimes referred to as de novo characterization. This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing a groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such populations in the population determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of the polymorphisms of the invention is described in the Examples section. The second type of analysis is determining which form(s) of a characterized polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15 mer at the 7 position; in a 16 mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, som example of which are described by WO 95/11995 (incorporated by reference in its entirety for all purposes). One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a diff rent array can be used for analysis of charact rized polymorphisms. WO 95/11995 also describes subarrays that

are optimized for detection of a variant forms of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first referenc sequence. The second group of probes is designed by the same principles as described in the Examples except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particular useful for analyzing short subsequences of the primary refer nce sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (*i.e.,* two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two primers leading to a detectable product signifying the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer. *See, e.g.,* WO 93/22456.

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual,* (Acad. Press, 1988)).

5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification,* (W.H. Freeman and Co, New York, 1992), Chapter 7.

6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence difference between alleles of target sequences.

III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. *See generally* National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed the lower the probability that the s t of polymorphic forms in one individual is the same as that in an unrelat d individual. Preferably, if multiple sit s ar analyzed, the sit s are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are diallelic because the population frequencies of two polymorphic forms can usually b determined with great r accuracy than thos of

multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying select d polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not th source of the sample. If the set of markers does match, one can conclude that the DNA from the susp ct is consistent with that found at the crime sc ne. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a match of suspect and crime scene sample would occur by chance.

B. Correlation of Polymorphisms with phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Some disease traits are already known to be mitochondrially inherited. Some such disease traits result, at least in part, from stop codons in structural genes. Such mutations have been mapped and associated with diseases, such as Leber's hereditary optic neuropathy, neurogenic muscular weakness, ataxia and retinitis pigmentosa. Other mutations (nucleotide substitutions) occur in tRNA coding sequences, and presumably cause conformational defects in transcribed tRNA molecules. Such mutations have also been mapped and associated with diseases such as Myoclonic Epilepsy and Ragged Red Fiber Disease. *See* Wallace, *Ann. Rev. Biochem.* 61, 1175-1212 (1992) (incorporated by reference in its entirety for all purposes).

Other genetic diseases having hitherto unmapped genetic component(s) may also result in part from variations in mitochondrial DNA. Candidate diseases include, e.g., agammaglobulimenia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria).

Other phenotypic traits that may derive, at least in part, from variations in mitochondrial DNA include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as Alzheimer's disease, autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic markers sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the individuals, some of whom exhibit a particular trait, and some of whom exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods such as a κ^2 squared test and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production in a mother after birth of a child.

Such correlations can be exploited in several ways. In the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediat administration of treatment, or at least th institution of r gular monitoring of the patient, before irretrievabl damage has occurred. Treatments include metabolic replacement and gene therapy. *See* Wallac , *supra*. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For exampl , the femal partner might elect

to undergo *in vitro* fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiven ss to one of several treatment regimes for a dis ase indicates that this treatment regim should be followed.

As an example of how mitochondrial polymorphisms can be correlated with phenotypic traits, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 If wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn=} \mu + YS_i + P_j + X_k + \beta_1 + \ldots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijknp} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise a segment of at least 10 bases of the nucleotide sequence of Anderson, supra, except at one of the polymorphic positions described in Table 1, column 1, in which the polymorphic position is occupied by a different base than described by Anderson, supra. Preferably, the different base is one of the alternative bases for that position shown in Table 1. Some nucleic acid encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences of proteins encoded by the nucleic acid sequence of Anderson, supra, (read in-frame) except at an amino acid encoded by a codon including one of the polymorphic positions shown in Table 1. That position is occupied by a different amino acid than described by Anderson, supra, and preferably an amino acid encoded by a corresponding codon of any of the alternative forms for the position shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, *e.g.*, mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, *i.e.*, 80, 95 or 99% free of cell component contaminants, as described in Jacoby, *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice,* 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology,* Vol. 182 (1990). If the prot in is secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

Th invention further provides transgenic nonhuman animals capabl of expressing an exogenous variant gen

and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. *See* Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10, 100 or all of the polymorphisms shown in Table 1. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

EXAMPLES

An array consisting of oligonucleotides complementary to subsequences of a target sequence can be used to determine the identity of a target sequence, measure its amount, and detect differences between the target and a reference sequence. Many different arrays can be designed for these purposes. One such design, termed a 4L tiled array, is depicted schematically in Fig. 1A. In each set of four probes, the perfect complement will hybridize more strongly than mismatched probes. By this approach, a nucleic acid target of length L can be scanned for mutations with a tiled array containing 4L probes. For example, to query the 16,569 bp of human mitochondrial DNA (mtDNA), only 66,276 probes of the possible 4^{10^9} 15-mers need to be used.

The use of a tiled array of probes to read a target sequence is illustrated in Fig. 1C. A tiled array of 15-mers varied at position 7 from the 3' end ($P^{15,7}$) was designed and synthesized for mt1, a cloned sequence containing 1,311 bp spanning the control region of mtDNA (Anderson, et al., *Nature* **290,** 457-465 (1981); Greenberg et al., *Gene* **21**, 33-49 (1983); Aquardo & Greenberg, *Genetics* **103,** 287-312 (1983); Cann et al. *Genetics* **106,** 479-499 (1984).

The mt1 and mt2 sequences were cloned from amplified genomic DNA extracted from hair roots (Gill et al. *Nature* **318**, 577-579 (1985); Saiki, et al., *Science* **239**, 487-491 (1988)). The clones were sequenced conventionally. Cloning was performed only to provide a set of pure reference samples of known sequence. To provide templates for fluorescent labeling, DNA was reamplified from the clones using primers bearing bacteriophage T3 and T7 RNA polymerase promoter sequences (bold; mtDNA sequences uppercase): L15935-T3, 5'ctc**ggaattaaccctcactaaagg**AAAC-CTTTTTCCAAGGA and H667-T7, 5'**taatacgactcactatagggag**AGGCTAGGACCAAACCTATT.

The upper panel of Fig. 1C shows a portion of the fluorescence image of an array hybridized with fluorescein-labeled mt1 RNA. Labeled RNAs from the two complementary 2mtDNA strands (designated L and H) were transcribed in separate reactions from a promoter-tagged PCR product. Each 10 µl reaction contained 1.5 mM each of ATP, CTP, GTP and UTP, 0.24 mM fluorescein-12-CTP (Du Pont), 0.24 mM fluorescein-12-UTP (Boehringer Mannh im), 1 to 5 nM (1.5 µl) crude unpurified 1.3 kb PCR product and 1 unit/ml T3 or T7 RNA polymerase (Promega), in a reaction buffer supplied with the enzyme. The reaction was carri d out at 37°C for 1 to 2 h. RNA was fragmented to an average

size of < 100 nt by adjusting the solution to 30 mM $MgCl_2$ by the addition of 1 M $MgCl_2$ and heating at 94°C for 40 minutes. Fragmentation improved the uniformity and specificity of hybridization. The extent of fragmentation is dependent on magnesium ion concentration [Huff et al., *Biochem.* **3**, 501-506 (1964); Butzow t al. *Biopolymers* **3**, 95-107 (1965)]. Good hybridization results have been obtained with both DNA and RNA targets prepared using a variety of labelling schemes, including incorporation of fluorescent and biotinylated dNTPs by DNA polymerases, incorporation of dye-labelled primers during PCR, ligation of labelled oligonucleotides to fragmented RNA, and direct labelling by photo-crosslinking a psoralen derivative of biotin directly to fragmented nucleic acids.

The base sequence can be read by comparing the intensities of the four probes within each column. For example, the column for position 16,493 consists of the four probes, 3' _TGACAT**A**GGCTGTAG, 3' TGACAT**C**GGCTGTAG, 3' TGACAT**G**GGCTGTAG, and 3' TGACAT**T**GGCTGTAG. The probe with the strongest signal is the probe with the **A** substitution (**A** 49, **C** 8, **G** 15, **T** 8 counts, 2 counts background), identifying the base at position 16,493 as U in the RNA transcript. Continuing the process, the sequence at each position can be read directly from the hybridization intensities.

The effect on the array hybridization pattern caused by a single base change in the target is shown in Fig. 1B, and the detection of a single-base polymorphism is shown in the lower panel of Fig. 1C. The target here is mt2, which differs from mt1 in this region by a T to C transition at position 16,493. Accordingly, the probe with the **G** substitution (third row) displays the strongest signal. Since the tiled array was designed to mt1, the hybridization intensities of neighboring probes that overlap 16,493 are also affected by the change in target sequence. The hybridization signals of 60 probes (4 x 15) of the 15-mer tiled array are perturbed by a single-base change in the target sequence. In the $P^{15,7}$ array, each probe querying the 8 positions to the left and 6 positions to the right of the polymorphism contain at least one mismatch to the target. The result is a characteristic loss of signal or a "footprint" for the probes flanking a mutation position. Of the four probes querying each position, the loss of signal is greatest for the one designed to match mt1. We denote the subset of probes with zero mismatches to the reference sequence as P^0.

A comparison of P^0 hybridization signals from a target to those from a reference is ideally obtained by hybridizing both samples to the same array. We therefore developed a two-color labeling and detection scheme in which the reference is labeled with phycoerythrin (red), and the target with fluorescein (green). The reference and unknown samples were labeled with biotin and fluorescein, respectively, in separate transcription reactions. Reactions were carried out as described above except that each contained 1.25 mM of ATP, CTP, GTP and UTP and 0.5 mM fluorescein-12-UTP or 0.25 mM biotin-16-UTP (Boehringer Mannheim). The two reactions were mixed in the ratio 1:5 (v/v) biotin: fluorescein and fragmented. Targets were diluted to a final concentration of 100 to 1000 pM in 3 M TMACl [Melchior et al., *Proc. Natl. Acad. Sci. USA* 70, 298-302 (1973)], 10 mM Tris.Cl pH 8.0, 1mM EDTA, 0.005% Triton X-100, and 0.2 nM of a control oligonucleotide, 5' fluorescein- CTGAACGGTAGCATCTTGAC. Samples were denatured at 95°C for 5 min, chilled on ice for 5 min and equilibrated to 37°C. A volume of 180 µl of hybridization solution was then added to the flow cell [Lipshutz et al., Biotechniques **19**, 442-447 (1995)], and the chip incubated at 37°C for 3 h with rotation at 60 rpm. The chip was washed 6 times at RT with 6xSSPE, 0.005% Triton X-100. Phycoerythrin-conjugated streptavidin (2 µg/ml in 6xSSPE, 0.005 % Triton X-100) was added and incubation continued at RT for 5 min. The chip was washed again, and rscanned at a resolution of ~ 74 pixels per probe cell. Two scans were collected, a fluorescein scan using a 515 to 545 nm bandpass filter, and a phycoerythrin scan using a 560 nm longpass filter. Signals were separated to remove spectral overlap and average counts per cell determined. By processing the reference and target together, experimental variability during the fragmentation, hybridization, washing, and detection steps is minimized or eliminated. In addition, during co-hybridization of the reference and target, competition for binding sites results in a slight improvement in mismatch discrimination. However, array hybridization is highly reproducible, and comparative analysis of data obtained from separate but identically synthesized arrays is also effective.

The two-color approach was tested by analyzing a 2.5 kb region of mtDNA, that spans the $tRNA^{Glu}$, cytochrome b, $tRNA^{Thr}$, $tRNA^{Pro}$, control region and $tRNA^{Phe}$ DNA sequences. Each 2.5 kb target sequence was PCR amplified directly from genomic DNA using the primer pair L14675-T3 (5'aattaaccctcactaaagggATTCTCGCACGGACTACAAC) and H667-T7. A $P^{20,9}$ array (i.e., containing 20-mer probes varied at position 9 from the 3' end) was designed to match the mt1 target (i.e., P^0 sequence = mt1). The mt1 reference (red) and a polymorphic target sample (green) were pooled and hybridized simultaneously to the array. Differences between the target and reference sequences were identified by comparing the scaled red and green P^0 hybridization intensities. To scale the sample to the reference intensities, a histogram of the base 10 logarithm of the intensity ratios for each pair of probes was constructed. The histogram had a mesh size of 0.01, and was smoothed by replacing the value at each point with the average number of counts over a five-point window centered at that point. The highest value in the histogram was located, and the resulting intensity ratio was taken to be the most probable calibration coefficient.

The marked decreas in target hybridization intensity, over a span of ~20 nucl otides, is shown for a single bas polymorphism at position 16,223 (Fig. 2A). The footprint is enlarged when two polymorphisms occur in close proximity (within ~20 nucleotides) as shown in Fig. 2B. When polymorphisms are clustered, the size of the footprint depends on the number of polymorphisms and their separation (Fig. 2C).

Polymorphisms, particularly multiple polymorphisms within a probe length, can be read most accurately by combining the results of basecalling and footprinting. Closely spaced multiple polymorphisms are easily identified by the presence of a large footprint (Fig. 2B and C) or by two or more basecalls differing from P^0 within a single probe span. Discrepancies between basecalling and footprint patterns are flagged for further analysis (for example, a P^0 footprint in which no polymorphism is identified: such a pattern is typical of a deletion). Thus, basecalls are valid only for unflagged regions. In flagged regions, the presence of sequence differences is detected, but no attempt is made to call the sequence without further analysis.

Sequence analysis was carried out on the 2.5 kb target from 12 samples. A total of 30,582 bp containing 180 substitutions relative to mt1 was analyzed. 98% of the sequence was unambiguously assigned by a Bayesian basecalling algorithm. Base identification was accomplished using a Bayesian classification algorithm based on variable kernel density estimation. The likelihood of each basecall associated with a set of hybridization intensity values was computed by comparing an unknown set of probes to a set of example cases for which the correct basecall was known. The resulting four likelihoods were then normalized so that they summed to 1. Data from both strands were combined by averaging the values. If the most likely basecall had an average normalized likelihood greater than 0.6, it was called, otherwise the base was called as an ambiguity. The example set was derived from 2 different samples, ib013 and ief005, which have a total of 35 substitutions relative to mt1, of which 19 are shared with the 12 samples analyzed and 16 are not. Basecalling performance was not sensitive to the choice of examples. Of this 98%, which contained both wild-type sequence and a high proportion of single-base footprints such as the example shown in Fig. 2A, 29,878 out of 29,879 bp were called correctly.

To provide an independently determined reference sequence, each 2.5 kb PCR amplicon was sequenced on both strands by primer-directed fluorescent chain-terminator cycle sequencing using an ABI 373A DNA sequencer, and assembled and manually edited using Sequencer 3.0. The analysis presented here assumes that the sequence amplified from genomic DNA is essentially clonal [Monnat & Loeb, *Proc. Natl. Acad. Sci. USA* **82**, 2895-2899 (1985)], and that its determination by gel-based methods is correct. A common length polymorphism at positions 303-309 was not detected by hybridization under the conditions used. It was excluded from analysis, and is not part of the set of 180 polymorphisms discussed in the text. However, polymorphisms at this site have previously been differentiated by oligonucleotide hybridization [Stoneking et al., *Am. J. Hum. Genet.* **48**, 370-382 (1991)].

The remaining 2%, that contained the multiple substitution footprints (such as those shown in Fig. 2B and 2C), was flagged for further analysis. Of the 649 bp comprising this 2%, 643 bp were located in or immediately adjacent to footprints. The P^0 intensity footprints were detected in the following way: the reference and sample intensities were normalized (15), and R, the average of $\log_{10}$ (P^0 reference / P^0 sample) over a window of 5 positions, centered at the base of interest, calculated for each position in the sequence. Footprints were detected as regions having at least 5 contiguous positions with a reference or sample intensity at least 50 counts above background, and an R value in the top 10th percentile for the experiment. At 205 polymorphic sites, where the sample was mismatched to P^0, the mean R value was 1.01, with a standard deviation of 0.57. At 35,333 non polymorphic sites (i.e. where both reference and sample had a perfect match to P^0) the mean value was -0.05, with a standard deviation of 0.25.

In all, 179 out of the 180 polymorphisms were unambiguously detected; 126 out of 127 were called correctly in the unflagged regions; and 53 polymorphisms occurring in the flagged regions were detected as footprints. There were no false positive basecalls, and only one false positive footprint. These figures can be considered to be "worst case" estimates for the type of array and target used. The P^0 sequence represents a Caucasian haplotype, and our sample set included 8 African samples having a large number of clustered differences to P^0. Furthermore, the variation in the hypervariable part of the control region is much higher than for the rest of the mitochondrial genome and for nuclear genes in general (Fig. 2A, B and C show comparisons to African samples in this region).

We therefore designed a $P^{25,13}$ tiling array for the mitochondrial genome. The array contains a total of 136,528 synthesis cells, each * 35 x 35 µm in size (Fig. 3). In addition to a 4L tiling across the genome, the array contains a set of probes representing a single base deletion at every position across the genome, and sets of probes designed to match a range of specific mtDNA haplotypes. Using long range PCR, the 16.6 kb mtDNA was amplified directly from genomic DNA samples. Long range PCR amplification was carried out on genomic DNA using Perkin Elmer GeneAmp XL PCR reagents according to the manufacturer's protocol. Primers were L14836-T3 (5'aattaaccctcactaaagggATGAAACTTCGGCTCACTCCTTGGC) and RH1066-T7 (5'taatacgactcactatagggaTTTCATCATGCGGAGATGTTGGATGG), based on RH 1066 [Cheng et al., *Nature Genetics* **7**, 350-351 (1994)]. Each 100 µl reaction contained 0.2 µM of each primer and 10-50 ng total genomic DNA. Transcription reactions were carried out using Ambion MAXIscript kit using the manufacturer's protocol. The concentration of the 16.6 kb PCR template was 2 nM and the reaction was spiked with 0.2 mM biotin-16-UTP. Incubation was at 37°C for 2 h. Fragmentation and hybridization were as described above, except that 3.5 M TMACl and 5' biotin-CTGAACGGTAGCATCTTGAC were used in the hybridization buffer, which also contained 100 µg/ml fragmented baker's yeast RNA (Sigma); and hybridization was carried out at 40°C for 4 h. Labelled RNA targets were prepared by in vitro transcription and hybridized to the array. Genomic hybridization patterns were imaged in less than 10 minutes by a high resolution confocal microscope.

A custom telocentric objective lens with a numerical aperture of 0.25 focuses 5 mW of 488 nm argon laser light to a 3 μm diameter spot, which is scanned by a galvanometer mirror across a 14 mm field at 30 lines/sec. Fluor scence collected by the objective is descann d by the galvanometer mirror, filtered by a dichroic beamsplitter (555 nm) and a bandpass filter (555-607 nm), focused onto a confocal pinhol , and detected by a photomultiplier. Photomultiplier output is digitized to 12 bits. A 4096 x 4096 pixel image is obtained in less than 3 min. Pixel size is 3.4 μm. The data from four sequential scans were summed to improve signal to noise.

Figure 3B shows the hybridization pattern of a 16.6 kb target to the mitochondrial genome chip. Although there ar some regions of low intensity, most of the 25-mer array hybridized efficiently: simply by identifying the highest intensity in each column of 4 substitution probes, 99.0 % of the mt3 sequence could be read correctly (P^0 sequence = mt3). The array was used to successfully detect three disease-causing mutations in a mitochondrial DNA sample from a patient suffering from Leber's hereditary optic neuropathy (Brown et al., *FASEB J.* **6**, 2791-2799 (1992)) (Fig. 3C). Furthermore, 7 errors and undetected polymorphisms from the gel-based sequence were identified.

We then hybridized 10 African genomes to the array and unambiguously identified 505 polymorphisms. These were polymorphisms that could be clearly read and for which a confirmatory footprint was detected automatically. For the 10 samples, the 2.5 kb cytochrome b and control region sequences were known. No false positives were detected in the 25 kb of sequence checked in this way. Additional clustered polymorphisms were detected by the presence of footprints, but not read directly.

The throughput of the system we describe is 5 chips per hour. Thus, 50 genomes can be read by hybridization in the time it takes to read 2 genomes conventionally. Furthermore, there are drastic reductions in sample preparation needs, because the entire genome is labeled in a single reaction, at a cost similar to that for a single sequencing reaction. Also, sequence reading at the level of data analysis is automated: the sequences can be read in a matter of minutes. No analytical separations or gel preparation are needed, which contributes to the speed of the experiment. Finally, a clear advantage to the approach we describe is that it is highly scalable. The cost, effort and time required to analyze the entire 16.6 kb mtDNA in a single experiment is virtually identical to that required to read 2.5 kb.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the diagnosis or monitoring of diseases, such as Alzheimer's disease, cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

Although the foregoing invention has been described in detail for purposes of clarity of understanding, it will be obvious that certain modifications may be practiced within the scope of the appended claims. All publications and patent documents cited above are hereby incorporated by reference in their entirety for all purposes to the same extent as if each were so individually denoted.

Table 1

pos	cbase	asm_base	HA001_v_me2	HA002_v_me2	HA004_v_me2	HA007_v_me2	IE013_v_me2	IEF002_v_me2	IEF005_v_me2	IEF007_v_me2	IEF011_v_me2	YF019
63	C	c	C	C	T	C	C	C	C	C	C	C
·72	G	a	G	G	A	G	G	G	G	G	G	G
92	A	a	A	g	G	G	A	A	A	A	A	A
181	C	c	T	T	c	T	c	t	C	C	C	C
194	T	t	c	C	t	C	t	c	T	C	C	C
234	G	a	A	A	g	A	a	A	A	A	A	A
246	G	g	G	G	A	G	a	G	G	G	G	G
296	A	a	A	A	A	A	G	A	A	A	A	A
315	G	g	G	G	G	G	A	G	G	G	G	G
324	C	c	C	T	C	T	C	C	C	C	C	C
662	G	a	A	A	A	A	A	A	A	A	A	A
679	T	t	T	C	T	C	T	T	T	T	T	T
708	G	g	A	A	G	A	G	A	G	G	G	G
768	G	g	A	a	a	a	a	A	G	A	A	a
824	T	t	T	T	A	T	A	T	T	T	T	T
1017	G	g	A	A	A	A	A	A	G	A	A	A
1039	T	t	T	T	T	C	T	T	T	T	T	T
1047	C	c	C	C	T	C	C	C	C	C	C	C
1441	G	g	A	A	G	A	G	A	G	G	G	G
1705	C	c	T	C	C	C	C	T	C	C	C	C
1735	G	a	A	A	A	A	A	A	A	A	A	A
2357	A	a	G	A	A	A	A	G	A	A	A	A
2415	T	t	t	t	T	t	T	A	T	n	t	t
2757	G	g	G	G	A	G	A	G	G	G	G	G

Table 1 continued

2788	C	c	C	C	C	C	C	C	C	T	T	T	
2884	T	t	T	T	C	T	C	T	T	T	T	T	
3009	G	g	G	G	G	G	G	G	G	G	G	A	
3199	T	t	T	A	T	A	T	T	T	T	T	T	
3335	T	t	T	T	T	T	T	T	T	T	C	T	
3336	G	g	G	A	G	G	G	G	G	G	G	G	
3449	C	c	C	C	C	C	C	C	T	C	C	C	
3515	C	c	C	C	A	C	C	C	C	C	C	C	
3593	C	c	T	T	T	t	c	T	C	T	T	T	
3647	C	c	T	C	C	C	C	C	C	C	C	C	
3665	G	g	G	G	G	G	A	G	G	G	G	G	
3744	G	g	G	A	G	G	G	G	G	G	G	G	
3865	T	t	T	T	C	T	T	T	T	T	T	T	
3917	G	g	G	G	G	G	G	G	G	A	A	G	
4103	A	a	G	G	G	G	G	G	A	G	G	G	
4157	A	a	G	A	A	A	A	G	A	A	A	A	
4247	C	t	T	T	T	T	T	T	T	T	T	T	
4311	C	c	C	C	T	C	C	C	C	C	C	C	
4585	T	t	T	T	C	T	T	T	T	T	T	T	
4766	A	a	G	A	A	A	A	G	A	A	A	A	
4823	G	a	A	A	A	A	A	A	A	A	A	A	
4966	T	t	T	T	T	C	T	T	T	T	T	T	
5026	C	c	T	C	C	C	C	T	C	C	C	C	
5095	T	t	T	T	C	T	T	T	T	T	T	T	
5146	G	g	G	G	G	G	G	G	G	G	A	G	
5230	G	g	G	G	A	G	G	G	G	G	G	G	
5251	G	g	G	G	G	G	G	G	G	G	G	A	
5284	A	a	A	A	A	A	A	A	A	g	G	A	
5330	C	c	A	C	C	C	C	A	C	C	C	C	
5459	G	g	G	G	A	G	G	G	G	G	G	G	
5602	C	c	C	C	T	C	C	C	C	C	C	C	
5772	G	g	G	G	G	G	G	G	A	G	G	G	
5813	T	t	C	T	T	T	T	C	T	T	T	T	
5822	A	a	A	A	A	G	A	A	A	A	A	A	
5911	C	c	T	C	C	C	C	C	C	C	C	C	
6070	T	t	T	T	T	T	C	T	T	T	T	T	
6149	G	g	G	G	G	G	A	G	G	G	G	G	
6236	C	c	C	C	C	C	C	C	T	C	C	C	
6252	T	t	T	T	T	C	T	T	T	T	T	T	
6526	G	a	A	A	A	A	A	A	A	A	A	A	
6613	T	t	C	T	T	T	T	C	T	T	T	T	
6662	A	a	A	A	A	A	A	A	A	A	A	G	
6712	C	c	T	C	C	C	C	T	C	C	C	C	
6805	A	a	G	A	A	A	A	G	A	A	A	A	
6826	T	t	T	C	T	T	T	T	T	T	T	T	
6874	C	c	C	C	C	C	C	C	C	A	C	C	
7145	A	a	A	A	G	A	G	A	A	A	A	A	
7174	T	t	T	T	T	T	T	T	T	C	C	C	
7255	C	c	T	T	T	T	T	T	C	T	T	T	
7273	C	c	C	C	C	C	C	C	C	T	T	T	
7388	T	t	T	T	T	T	C	T	T	T	T	T	
7517	A	a	A	r	A	G	a	a	A	N	A	A	
7520	G	g	A	c	A	G	g	g	G	A	A	A	

Table 1 continued

7623	T	t	A	A	T	A	T	A	T	T	T	T	
7770	A	a	A	A	A	A	A	A	A	G	G	G	
8026	A	g	G	G	G	G	A	G	G	G	G	G	
8079	C	c	T	C	C	C	C	T	C	C	C	C	
8205	G	g	A	A	G	A	G	A	G	A	A	A	
8386	G	g	A	G	G	G	G	A	G	G	G	G	
8427	C	c	C	C	T	C	C	C	C	C	C	C	
8467	C	c	C	C	T	C	T	C	C	C	C	C	
8502	T	t	C	T	T	C	T	C	T	T	T	T	
8565	A	a	A	A	G	A	A	A	A	A	A	A	
8654	C	c	C	C	T	C	T	C	C	C	C	C	
8700	A	a	G	G	G	G	G	G	G	G	G	G	
8783	A	a	A	A	A	A	G	A	A	A	A	A	
8793	T	c	C	C	C	C	C	C	C	C	C	C	
8853	G	g	G	G	G	G	G	G	G	G	G	A	
8876	T	t	T	T	T	T	C	T	T	T	T	T	
9041	C	c	C	C	T	C	C	C	C	C	C	C	
9071	A	a	A	A	A	A	G	A	A	A	A	A	
9220	A	a	G	G	A	G	A	G	A	G	G	G	
9346	A	a	A	A	G	A	A	A	A	A	A	A	
9448	C	c	C	C	C	C	C	C	T	C	C	C	
9817	C	c	C	C	T	C	C	C	C	C	C	C	
10030	T	t	T	T	T	T	C	T	T	T	T	T	
10114	T	t	C	C	T	C	T	C	T	C	C	T	
10320	T	t	T	T	T	T	C	T	T	T	T	T	
10372	G	g	G	G	G	G	G	G	A	G	G	G	
10585	G	g	G	G	g	G	A	G	G	G	G	G	
10663	C	c	C	C	T	C	C	C	C	C	C	C	
10687	G	g	G	G	A	G	A	G	G	G	G	G	
10792	C	c	C	C	C	C	T	C	C	T	C	C	
10809	T	t	T	T	C	T	C	T	T	T	T	T	
10827	T	t	T	T	T	T	C	T	T	T	T	T	
10872	T	t	C	C	C	C	C	C	T	C	C	C	
10914	T	t	T	T	C	T	T	T	T	T	t	T	
11163	A	a	A	A	A	A	G	A	A	A	A	A	
11175	A	g	G	G	A	G	G	G	G	G	G	G	
11640	A	a	A	A	G	A	A	A	A	A	A	A	
11653	A	a	A	A	A	A	G	A	A	A	A	A	
11799	A	a	A	A	A	A	A	A	G	A	A	A	
11913	G	g	G	G	A	G	G	G	G	A	A	A	
11943	T	t	C	C	T	C	T	C	T	C	C	G	
12006	A	g	G	G	A	G	G	G	G	G	G	G	
12048	C	c	C	C	C	C	T	C	C	C	C	C	
12114	C	c	C	C	C	C	T	C	C	C	C	C	
12235	G	g	A	A	G	A	G	A	G	G	G	G	
12353	T	t	T	T	T	T	T	T	T	T	T	C	
12476	T	t	T	T	T	T	C	T	T	T	T	T	
12719	A	a	A	A	G	A	A	A	A	A	A	A	
12776	A	a	G	A	A	A	A	A	A	A	A	A	
12809	A	a	A	A	A	A	G	A	A	A	A	A	
12947	A	a	G	A	A	A	A	G	A	A	A	A	
13104	A	a	A	A	G	A	G	A	G	A	A	A	
13148	A	a	A	A	A	A	G	A	A	A	A	A	

Table 1 continued

13183	T	t	T	T	T	C	T	T	T	T	T	T	
13202	A	a	A	A	A	G	A	A	A	A	A	A	
13275	A	a	A	A	G	A	A	A	A	A	A	A	
13484	A	a	A	A	A	A	G	A	A	A	A	A	
13505	C	c	C	C	T	C	t	C	C	C	C	C	
13589	G	g	a	A	G	A	G	A	G	A	A	A	
13649	C	c	t	t	t	t	T	T	C	T	T	t	
13788	T	t	T	T	T	T	C	T	T	T	t	T	
13802	A	a	A	A	A	A	A	A	A	g	G	g	
13913	C	c	C	C	C	C	C	C	A	C	C	C	
13957	G	g	G	C	G	C	G	G	G	G	G	G	
13965	A	a	G	A	A	A	A	G	A	A	A	A	
13999	T	t	T	T	T	T	A	T	T	T	T	T	
14058	A	a	G	A	A	A	A	G	A	A	A	A	
14177	T	t	T	T	T	T	C	T	T	T	T	T	
14307	T	t	T	T	C	T	T	T	T	T	T	T	
14406	C	c	T	C	C	C	C	T	C	C	C	C	
14559	G	g	G	G	G	G	A	G	G	G	G	G	
14565	A	a	A	A	A	A	A	A	A	G	G	G	
14910	C	c	C	C	C	C	T	C	C	C	C	C	
15042	G	g	G	G	G	A	G	G	G	G	G	G	
15066	T	t	T	T	T	T	C	T	T	T	T	T	
15109	G	g	A	A	G	A	G	A	G	G	G	G	
15118	G	g	G	G	G	G	G	G	G	G	G	A	
15135	C	c	C	C	T	C	C	C	C	C	C	C	
15216	G	g	A	A	G	A	G	A	G	G	G	G	
15243	A	a	A	A	A	A	A	A	A	G	G	A	
15300	G	g	A	A	G	A	G	A	a	A	A	A	
15430	G	g	G	G	A	G	G	G	G	G	G	G	
15628	T	t	T	T	T	T	T	T	T	C	C	T	
15733	G	g	G	G	G	G	G	G	G	G	G	A	
15783	T	t	T	T	T	T	T	T	T	C	C	C	
15848	C	c	C	T	C	T	C	C	C	C	C	C	
15882	G	g	G	G	G	G	G	G	A	G	G	G	
15901	A	a	A	A	A	A	A	A	G	A	A	A	
16092	T	t	T	T	T	T	C	T	T	T	T	T	
16110	T	c	C	C	C	C	C	C	C	C	C	C	
16113	C	c	A	C	C	C	C	A	C	C	C	C	
16123	T	t	t	T	T	T	T	T	C	T	T	T	
16125	T	t	t	T	T	T	T	T	T	T	C	T	
16128	G	g	A	G	A	G	G	G	G	G	G	G	
16144	G	g	G	G	G	G	G	A	G	G	G	G	
16147	C	c	C	C	T	C	C	C	C	C	C	C	
16263	C	c	C	C	C	T	c	C	C	C	c	C	
16277	C	c	T	T	C	T	t	T	T	t	T	T	
16289	T	c	C	C	C	C	t	C	C	t	c	c	
16317	A	a	A	G	a	A	A	A	A	A	A	A	
16318	A	g	G	G	g	G	G	G	G	G	G	G	
16353	C	c	T	C	C	C	C	T	C	C	C	C	
16361	C	t	T	T	C	T	T	T	C	T	T	T	
16389	G	g	A	a	G	a	G	A	G	A	A	A	
16518	T	t	T	T	C	T	c	T	C	C	C	C	

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Affymetrix, Inc
3380 Central Expressway
Santa Clara
CA 95051
US

(ii) TITLE OF INVENTION: Polymorphisms in Human Mitochondrial Nucleic Acid

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:
Hepworth Lawrence Bryer & Bizley
Merlin House
Falconry Court
Baker's Lane
Epping
Essex CM16 5DQ
UK

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: EPA 97 303327.7
(B) FILING DATE: 16-MAY-1997

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/017,203
(B) FILING DATE: 16-AUG-1996

(A) APPLICATION NUMBER: US 60/024,206
(B) FILING DATE: 20-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: BIZLEY, Richard Edward
(B) REFERENCE/DOCKET NUMBER: APEP97617

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: +44 (0)1992 561756
(B) TELEFAX: +44 (0)1992 561934

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGGAATTA ACCCTCACTA AAGGAAACCT TTTTCCAAGG A 41

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TAATACGACT CACTATAGGG AGAGGCTAGG ACCAAACCTA TT 42

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGACATAGGC TGTAG 15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGACATCGGC TGTAG 15

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGACATGGGC TGTAG 15

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGACATTGGC TGTAG 15

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGAACGGTA GCATCTTGAC 20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AATTAACCCT CACTAAAGGG ATTCTCGCAC GGACTACAAC 40

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AATTAACCCT CACTAAAGGG ATGAAACTTC GGCTCACTCC TTGGC 45

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TAATACGACT CACTATAGGG ATTTCATCAT GCGGAGATGT TGGATGG 47

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGAACGGTA GCATCTTGAC 20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGAACTGTAT CCGACAT 17

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGACATGGCT GTAG 14

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGACATGGGC TGTAG 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGACATGGGC TGTAG 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGACATTGGC TGTAG 15

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACATAAGCT GTAGA 15

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GACATACGCT GTAGA 15

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GACATAGCTG TAGA 14

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GACATATGCT GTAGA 15

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGAACTGTAC CCGACAT 17

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGACATAGGC TGTAG 15

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGACATCGGC TGTAG 15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGACATGGCT GTAG 14

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGACATTGGC TGTAG 15

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GACATAAGCT GTAGA 15

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACATACGCT GTAGA 15

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GACATAGCTG TAGA 14

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GACATATGCT GTAGA 15

Claims

1. A segment of human mitochondrial DNA or RNA of between 10 and 100 bases including any one of the polymorphic sites shown in Table 1, or the complement of the segment.

2. The segment of claim 1, wherein the polymorphic form occupying the polymorphic site is listed in Table 1, column 3.

3. The segment of claim 1, wherein the polymorphic form cccupying the polymorphic site is an alternative form listed in Table 1, column 2, or 4-11.

4. An allele-specific oligonucleotide that hybridizes to a segment of human mitochondrial nucleic acid or its complement including a polymorphic site shown in Table 1, column 1.

5. The allele-specific oligonucleotide of claim4 that is probe.

6. The allele-specific oligonucleotide of claim 5, wherein a central position of the probe aligns with the polymorphic site of the fragment.

7. The allele-specific oligonuclectide of claim4 that is a primer.

8. The allele-specific oligonucleotide of claim 7, wherein the 3' end of the primer aligns with the polymorphic site of the fragment.

9. An isolated nucleic acid comprising a segment of the human mitochondrial sequence described by Anderson et al., *Nature* 290, 457-465 (1981), or the complement thereof, including a polymorphic site shown in Table 1, column 1, wherein the polymorphic site within the segment is cccupied by a base other than the base shown in Table 1, column 3 ("asn base").

10. A method of analyzing a nucleic acid, comprising:

    obtaining the nucleic acid from an individual; and
    determining a base occupying any one of the polymorphic sites shown in Table 1.

Figure 1

A

```
5' ..TGAACTGTATCCGACAT..
3'      tgacat ggctgtag
        tgacatCggctgtag
        tgacatGggctgtag
        tgacatTggctgtag
3'       gacataAgctgtaga
         gacataCgctgtaga
         gacata gctgtaga
         gacataTgctgtaga
```

B

```
5' ..TGAACTGTACCCGACAT..
3'      tgacatAggctgtag
        tgacatCggctgtag
        tgacat ggctgtag
        tgacatTggctgtag
3'       gacataAgctgtaga
         gacataCgctgtaga
         gacata gctgtaga
         gacataTgctgtaga
```

C

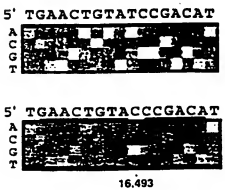


Figure 2

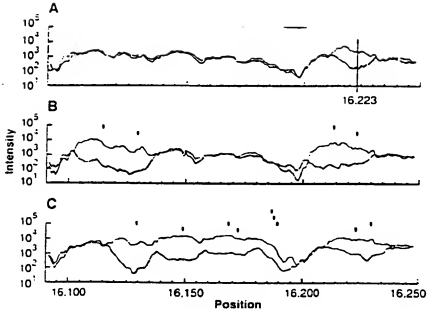
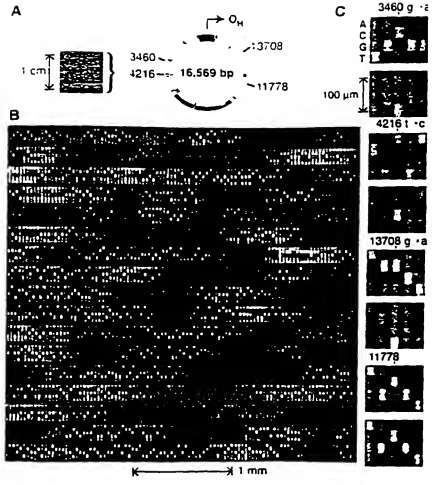


Figure 3


A
B
C
O_H
3708
3460
4216
16,569 bp
11778
1 cm
100 µm
1 mm
3460 g
4216 t
13708 g
11778